

Amendments to the Specification:

Please replace the paragraph appearing on page 14, lines 7-31 of the specification with the following amended paragraph:

The term "identity" refers to the relatedness of two sequences on a nucleotide-by-nucleotide basis over a particular comparison window or segment. Thus, identity is defined as the degree of sameness, correspondence or equivalence between the same strands (either sense or antisense) of two DNA segments. "Percentage of sequence identity" is calculated by comparing two optimally aligned sequences over a particular region, determining the number of positions at which the identical base occurs in both sequence in order to yield the number of matched positions, dividing the number of such positions by the total number of positions in the segment being compared and multiplying the result by 100. Optimal alignment of sequences may be conducted by the algorithm of Smith & Waterman, Appl. Math. 2:482 (1981), by the algorithm of Needleman & Wunsch, J. Mol. Biol. 48:443 (1970), by the method of Pearson & Lipman, Proc. Natl. Acad. Sci. (USA) 85:2444 (1988) and by computer programs which implement the relevant algorithms (e.g., Clustal Macaw Pileup [<http://cmgm.stanford.edu/biochem218/11Multiple.pdf>]; Higgins et al., CABIOS. 5L151-153 (1989)), FASTDB (Intelligenetics), BLAST (National Center for Biomedical Information; Altschul et al., Nucleic Acids Research 25:3389-3402 (1997)), PILEUP (Genetics Computer Group, Madison, WI) or GAP, BESTFIT, FASTA and TFASTA (Wisconsin Genetics Software Package Release 7.0,

Genetics Computer Group, Madison, WI). (See U.S. Patent No. 5,912,120.)

Please replace the paragraph appearing on page 65, lines 15-28 of the specification with the following amended paragraph:

The goal of this experiment was to isolate the delta 12-desaturase gene from *S. diclina* and verify its functionality by expressing the enzyme in a heterologous host system such as yeast. The approach taken was to design degenerate primers (oligonucleotides) that represent conserved amino acid motifs from known delta 12-desaturases. In designing these primers, known delta-12 desaturase sequence information from both fungi and plant sources was used, including sequence information from: *Mortierella alpina* (Accession #AF110509), *Mucor rouxii* (Accession #AF161219), *Brassica juncea* (Accession #X91139), *Arabidopsis thaliana* (Accession #L26296), and *Borago officinalis* (Accession #AF0744324). The sequence information was analyzed using the CODEHOP Blockmaker program [<http://blocks.fhcrc.org/codehop.html>].